

mays=corn, Transposon Mutant, 150 nt]

```
Seq. No.      297846
Seq. ID       LIB3150-050-Q1-N1-H11
Method        BLASTX
NCBI GI       g1885348
BLAST score   159
E value       3.0e-11
Match length  47
% identity    77
NCBI Description (X91515) histone H4 [Trichogramma caceociae]
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Seq. No.      297847
Seq. ID      LIB3150-050-Q1-N1-H9
Method       BLASTX
NCBI GI      g1346251
BLAST score   208
E value      2.0e-16
Match length  53
% identity    79
NCBI Description  HISTONE H2B.4 >gi_577819_emb_CAA49585_ (X69961) H2B histone
[Zea mays]
```

```
Seq. No.      297848
Seq. ID      LIB3150-051-Q1-N1-B9
Method       BLASTX
NCBI GI      g1709000
BLAST score   422
E value      1.0e-41
Match length  88
% identity    92
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
>gi_960357_dbj_BAA09895_(D63835) S-adenosylmethionine
synthetase [Hordeum vulgare]
```

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Seq. No.      297849
Seq. ID      LIB3150-051-Q1-N1-C10
Method       BLASTX
NCBI GI      g133961
BLAST score   260
E value      1.0e-22
Match length  68
% identity    78
NCBI Description  40S RIBOSOMAL PROTEIN S4 (OMNIPOTENT SUPPRESSOR PROTEIN
SUP44) (RP12) (S2E) >gi_70888_pir_R3BYS2 ribosomal protein
S2.e - yeast (Saccharomyces cerevisiae) >gi_172793 (M59375)
ribosomal protein S4 [Saccharomyces cerevisiae]
>gi_1322683_emb_CAA96831_ (Z72645) ORF YGL123w
[Saccharomyces cerevisiae] >gi_1628451_emb_CAA63835_
(X94106) SUP44 [Saccharomyces cerevisiae]
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Seq. No.      297850
Seq. ID      LIB3150-051-Q1-N1-C7
Method       BLASTX
NCBI GI      g3334756
BLAST score   224
```


E value 7.0e-59
Match length 108
% identity 100
NCBI Description (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC4 [Zea mays]

Seq. No. 297896
Seq. ID LIB3150-059-Q1-N1-C11
Method BLASTX
NCBI GI g133867
BLAST score 258
E value 1.0e-22
Match length 83
% identity 64
NCBI Description 40S RIBOSOMAL PROTEIN S11 >gi_82722_pir_S16577 ribosomal protein S11 - maize >gi_22470_emb_CAA39438_ (X55967) ribosomal protein S11 [Zea mays]

Seq. No. 297897
Seq. ID LIB3150-059-Q1-N1-C8
Method BLASTX
NCBI GI g134613
BLAST score 321
E value 9.0e-30
Match length 74
% identity 84
NCBI Description SUPEROXIDE DISMUTASE-2 (CU-ZN) >gi_82727_pir_A29077 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) 2 - maize >gi_168620 (M54936) superoxide dismutase 2 [Zea mays] >gi_168622 (M15175) SOD2 protein [Zea mays]

Seq. No. 297898
Seq. ID LIB3150-059-Q1-N1-D10
Method BLASTX
NCBI GI g129916
BLAST score 238
E value 3.0e-20
Match length 60
% identity 80
NCBI Description PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir_TVWTGY phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat >gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase (AA 1 - 401) [Triticum aestivum]

Seq. No. 297899
Seq. ID LIB3150-059-Q1-N1-D11
Method BLASTX
NCBI GI g3334138
BLAST score 269
E value 5.0e-28
Match length 94
% identity 66
NCBI Description CALNEXIN HOMOLOG PRECURSOR >gi_669003 (U20502) calnexin [Glycine max]

Seq. No. 297900
Seq. ID LIB3150-059-Q1-N1-D12

[illegible]

Seq. No.	297917
Seq. ID	LIB3150-064-P2-K1-G2
Method	BLASTN
NCBI GI	g1184775
BLAST score	40
E value	2.0e-13
Match length	72
% identity	89
NCBI Description	Zea mays glyceraldehyde-3-phosphate dehydrogenase GAPC4 (gpc4) mRNA, complete cds

Seq. No.	297918
Seq. ID	LIB3150-064-P2-K1-H6
Method	BLASTN
NCBI GI	g606969
BLAST score	35
E value	2.0e-10
Match length	71
% identity	87
NCBI Description	Arabidopsis thaliana cytoplasmic ribosomal protein L18 mRNA, complete cds

```
Seq. No.      297919
Seq. ID      LIB3150-065-P2-K1-A3
Method       BLASTX
NCBI GI      g1321661
BLAST score   154
E value      3.0e-10
Match length  39
% identity    79
NCBI Description (D45423) ascorbate peroxidase [Oryza sativa]
```

41812

Method BLASTX
 NCBI GI g82512
 BLAST score 171
 E value 2.0e-12
 Match length 37
 % identity 47
 NCBI Description ubiquitin precursor - rice (fragment)
 >gi_218189_dbj_BAA02241_ (D12776) poly-ubiquitin [Oryza
 sativa]

Seq. No. 297937
 Seq. ID LIB3150-067-P1-N1-G4
 Method BLASTN
 NCBI GI g22176
 BLAST score 163
 E value 1.0e-86
 Match length 289
 % identity 89
 NCBI Description Z.mays P gene

Seq. No. 297938
 Seq. ID LIB3150-067-P2-K1-A6
 Method BLASTX
 NCBI GI g2511531
 BLAST score 197
 E value 9.0e-16
 Match length 49
 % identity 73
 NCBI Description (AF008120) alpha tubulin 1 [Eleusine indica]
 >gi_3163944_emb_CAA06618_ (AJ005598) alpha-tubulin 1
 [Eleusine indica]

Seq. No. 297939
 Seq. ID LIB3150-067-P2-K1-B12
 Method BLASTN
 NCBI GI g2286150
 BLAST score 151
 E value 3.0e-79
 Match length 331
 % identity 85
 NCBI Description Zea mays translation initiation factor (eIF-4A) mRNA,
 complete cds

Seq. No. 297940
 Seq. ID LIB3150-067-P2-K1-D4
 Method BLASTN
 NCBI GI g168482
 BLAST score 95
 E value 3.0e-46
 Match length 159
 % identity 91
 NCBI Description Corn starch branching enzyme II mRNA, complete cds

Seq. No. 297941
 Seq. ID LIB3150-067-P2-K1-D6
 Method BLASTN
 NCBI GI g2668741

BLAST score 165
E value 7.0e-88
Match length 248
% identity 92
NCBI Description Zea mays glycine-rich RNA binding protein (GRP) mRNA, complete cds

Seq. No. 297942
Seq. ID LIB3150-067-P2-K1-F3
Method BLASTX
NCBI GI g1172836
BLAST score 169
E value 3.0e-12
Match length 46
% identity 76
NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN-B1 >gi_496272 (L16787) small ras-related protein [Nicotiana tabacum]

Seq. No. 297943
Seq. ID LIB3150-067-P2-K1-G2
Method BLASTX
NCBI GI g4096786
BLAST score 168
E value 7.0e-12
Match length 35
% identity 94
NCBI Description (U39958) NADP-malic enzyme [Zea mays]

Seq. No. 297944
Seq. ID LIB3150-068-P1-N1-B6
Method BLASTX
NCBI GI g4467099
BLAST score 221
E value 4.0e-18
Match length 72
% identity 71
NCBI Description (AL035538) glycine hydroxymethyltransferase like protein [Arabidopsis thaliana]

Seq. No. 297945
Seq. ID LIB3150-068-P1-N1-C2
Method BLASTX
NCBI GI g1184774
BLAST score 271
E value 5.0e-24
Match length 74
% identity 78
NCBI Description (U45856) cytosolic glyceraldehyde-3-phosphate dehydrogenase GAPC3 [Zea mays]

Seq. No. 297946
Seq. ID LIB3150-068-P1-N1-C5
Method BLASTX
NCBI GI g1709619
BLAST score 280
E value 5.0e-25
Match length 57


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Match length      102
% identity        35
NCBI Description  DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR
                  >gi_479589_pir_S34823 dehydration-induced protein RD22 -
                  Arabidopsis thaliana >gi_391608_dbj_BAA01546_(D10703) rd22
                  [Arabidopsis thaliana] >gi_447134_prf_1913421A rd22 gene
                  [Arabidopsis thaliana]

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```
Seq. No.      297992
Seq. ID      LIB3150-073-P2-K1-B10
Method       BLASTN
NCBI GI      g4185305
BLAST score   43
E value      6.0e-15
Match length  207
% identity    81
NCBI Description Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
                  (sz22-21) gene, complete cds; retrotransposon Opie-2 gag
                  protein, polypeptide, and copia protein genes, complete
                  cds; and unknown genes
```

Seq. No.	297993
Seq. ID	LIB3150-073-P2-K1-B3
Method	BLASTX
NCBI GI	g3745759
BLAST score	195
E value	6.0e-15
Match length	56
% identity	70
NCBI Description	Chain B, X-Ray Structure Of The Nucleosome Core Particle At 2.8 A Resolution >gi_3745763_pdb_1AOI_F Chain F, X-Ray Structure Of The Nucleosome Core Particle At 2.8 A Resolution

```
Seq. No.      297994
Seq. ID      LIB3150-073-P2-K1-B8
Method      BLASTN
NCBI GI      g2286150
BLAST score   263
E value      1.0e-146
Match length  275
% identity    99
NCBI Description Zea mays translation initiation factor (eIF-4A) mRNA,
                complete cds
```

Seq. No.	297995
Seq. ID	LIB3150-073-P2-K1-C4
Method	BLASTX
NCBI GI	g2182029
BLAST score	233
E value	2.0e-19
Match length	89
% identity	57
NCBI Description	(Y13437) shaggy-like kinase etha (OSKetha) [Oryza sativa]

Seq. No.	297996
Seq. ID	LIB3150-073-P2-K1-C9

[illegible]

Seq. No.

Seq. No.

Seq. No.

Seq. No.

protein homolog from Arabidopsis thaliana BAC gb_AC003673.
[Arabidopsis thaliana]

Seq. No. 298017
Seq. ID LIB3150-075-P2-N2-H11
Method BLASTX
NCBI GI g4220445
BLAST score 171
E value 1.0e-12
Match length 73
% identity 47
NCBI Description (AC006216) Similar to gi_3004555 F19F24.14 salt inducible protein homolog from Arabidopsis thaliana BAC gb_AC003673.
[Arabidopsis thaliana]

Seq. No. 298018
Seq. ID LIB3150-075-P2-N2-H12
Method BLASTX
NCBI GI g1730666
BLAST score 169
E value 7.0e-12
Match length 70
% identity 54
NCBI Description HYPOTHETICAL 32.2 KD PROTEIN IN ARE2-SWP73 INTERGENIC REGION >gi_2131968_pir_S63351 hypothetical protein YNR020c - yeast (Saccharomyces cerevisiae)
>gi_1302506_emb_CAA96299_ (Z71635) ORF YNR020c
[Saccharomyces cerevisiae]

Seq. No. 298019
Seq. ID LIB3150-076-P1-N1-F3
Method BLASTX
NCBI GI g4582468
BLAST score 150
E value 7.0e-10
Match length 64
% identity 47
NCBI Description (AC007071) putative 40S ribosomal protein; contains C-terminal domain [Arabidopsis thaliana]

Seq. No. 298020
Seq. ID LIB3150-076-P1-N1-G3
Method BLASTX
NCBI GI g1184776
BLAST score 280
E value 4.0e-25
Match length 71
% identity 79
NCBI Description (U45857) cytosolic glyceraldehyde-3-phosphate dehydrogenase GAPC4 [Zea mays]

Seq. No. 298021
Seq. ID LIB3150-076-P2-N2-A7
Method BLASTX
NCBI GI g3337352
BLAST score 331
E value 4.0e-31

Match length	131
% identity	56
NCBI Description	(AC007017) putative transcription factor E2F5 [Arabidopsis thaliana]
Seq. No.	298062
Seq. ID	LIB3150-079-P1-N1-E7
Method	BLASTX
NCBI GI	g730558
BLAST score	225
E value	6.0e-28
Match length	96
% identity	74
NCBI Description	60S RIBOSOMAL PROTEIN L34 >gi_1076636_pir__S48027 ribosomal protein L34 - common tobacco >gi_2129964_pir__S48028 ribosomal protein L34.e, cytosolic - common tobacco >gi_436030 (L27089) 60S ribosomal protein L34 [Nicotiana tabacum] >gi_436032 (L27107) 60S ribosomal protein L34 [Nicotiana tabacum]
Seq. No.	298063
Seq. ID	LIB3150-079-P2-N2-A11
Method	BLASTN
NCBI GI	g3318612
BLAST score	78
E value	6.0e-36
Match length	190
% identity	84
NCBI Description	Zea mays mRNA for mitochondrial phosphate transporter, complete cds
Seq. No.	298064
Seq. ID	LIB3150-079-P2-N2-B1
Method	BLASTN
NCBI GI	g416263
BLAST score	37
E value	2.0e-11
Match length	65
% identity	89
NCBI Description	Rice mRNA for ribosomal protein S28, partial sequence
Seq. No.	298065
Seq. ID	LIB3150-079-P2-N2-E4
Method	BLASTN
NCBI GI	g1213278
BLAST score	60
E value	3.0e-25
Match length	100
% identity	90
NCBI Description	Z.mays ZEMb gene
Seq. No.	298066
Seq. ID	LIB3150-079-P2-N2-F3
Method	BLASTX
NCBI GI	g3805847
BLAST score	315
E value	5.0e-29

[illegible]

```
Seq. No.      298076
Seq. ID      LIB3150-082-P1-N1-B8
Method       BLASTN
NCBI GI      g28111133
BLAST score   100
E value      4.0e-49
Match length  189
% identity    88
NCBI Description  Zea mays starch synthase isoform zSTSII-1 (zSSIIa) mRNA,
partial cds
```


alpha chain - maize >gi_1321656_dbj_BAA08249_ (D45408)
alpha subunit of translation elongation factor 1 [Zea mays]

Seq. No. 298088
Seq. ID LIB3150-083-P2-N2-A10
Method BLASTX
NCBI GI g4406372
BLAST score 188
E value 3.0e-14
Match length 43
% identity 77
NCBI Description (AF109156) thiosulfate sulfurtransferase [Datisca glomerata]

Seq. No. 298089
Seq. ID LIB3150-083-P2-N2-C12
Method BLASTN
NCBI GI g1575127
BLAST score 220
E value 1.0e-120
Match length 280
% identity 94
NCBI Description Zea mays luminal binding protein cBiPe2 mRNA, complete cds

Seq. No. 298090
Seq. ID LIB3150-083-P2-N2-D11
Method BLASTN
NCBI GI g531055
BLAST score 64
E value 1.0e-27
Match length 72
% identity 97
NCBI Description Wheat mRNA for protein H2B-6, complete cds

Seq. No. 298091
Seq. ID LIB3150-083-P2-N2-F12
Method BLASTX
NCBI GI g2760321
BLAST score 309
E value 2.0e-28
Match length 108
% identity 59
NCBI Description (AC002130) F1N21.6 [Arabidopsis thaliana]

Seq. No. 298092
Seq. ID LIB3150-083-P2-N2-G11
Method BLASTX
NCBI GI g480450
BLAST score 158
E value 1.0e-10
Match length 34
% identity 91
NCBI Description ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis thaliana >gi_402552_emb_CAA49506_ (X69880) ketol-acid reductoisomerase [Arabidopsis thaliana]

Seq. No. 298093



cds

Seq. No. 298109
 Seq. ID LIB3150-087-P2-K1-G2
 Method BLASTN
 NCBI GI g22121
 BLAST score 191
 E value 1.0e-103
 Match length 243
 % identity 95
 NCBI Description Maize alcohol dehydrogenase 1 gene (Adh1-1F)

Seq. No. 298110
 Seq. ID LIB3150-088-P2-K1-A4
 Method BLASTN
 NCBI GI g22272
 BLAST score 105
 E value 7.0e-52
 Match length 328
 % identity 82
 NCBI Description Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)

Seq. No. 298111
 Seq. ID LIB3150-088-P2-K1-B10
 Method BLASTX
 NCBI GI g3928086
 BLAST score 157
 E value 2.0e-10
 Match length 45
 % identity 58
 NCBI Description (AC005770) unknown protein [Arabidopsis thaliana]

Seq. No. 298112
 Seq. ID LIB3150-088-P2-K1-D11
 Method BLASTX
 NCBI GI g4586035
 BLAST score 147
 E value 3.0e-10
 Match length 89
 % identity 48
 NCBI Description (AC007109) putative prohibitin protein [Arabidopsis thaliana]

Seq. No. 298113
 Seq. ID LIB3150-088-P2-K1-F2
 Method BLASTX
 NCBI GI g4115937
 BLAST score 226
 E value 2.0e-18
 Match length 51
 % identity 75
 NCBI Description (AF118223) contains similarity to human PCF11p homolog (GB:AF046935) [Arabidopsis thaliana]

Seq. No. 298114
 Seq. ID LIB3150-089-P1-N1-B10
 Method BLASTX


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Seq. No.      298130
Seq. ID      LIB3150-091-P1-N1-F1
Method       BLASTN
NCBI GI      g2431768
BLAST score   64
E value      2.0e-27
Match length 160
% identity   85
NCBI Description Zea mays acidic ribosomal protein Pl1a (rppla) mRNA,
                  complete cds
```

```
Seq. No.      298131
Seq. ID      LIB3150-091-P1-N1-G4
Method       BLASTX
NCBI GI      g3236242
BLAST score   176
E value      8.0e-13
Match length 100
% identity   45
NCBI Description (AC004684) putative ribosomal protein L36 [Arabidopsis
thaliana]
```

```
Seq. No.      298132
Seq. ID      LIB3150-091-P1-N1-G7
Method       BLASTX
NCBI GI      g1174613
BLAST score   162
E value      1.0e-14
Match length  84
% identity    57
NCBI Description  26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING
PROTEIN HOMOLOG 1) (TBP-1) >gi_556560_dbj_BAA04614_
(D17788) rice homologue of Tat binding protein [Oryza
sativa]
```

```
Seq. No.      298133
Seq. ID      LIB3150-092-P1-N1-B1
Method       BLASTX
NCBI GI      g462243
BLAST score   208
E value      1.0e-16
Match length  85
% identity    61
NCBI Description HISTONE H4 >gi_421921_pir_S32769 histone H4 - tomato
                >gi_297150_emb_CAA48923_(X69179) histone H4 [Lycopersicon
                esculentum] >gi_297152_emb_CAA48924_(X69180) histone H4
                [Lycopersicon esculentum] >gi_2746721_(AF038387) histone H4
                [Capsicum annuum]
```

```
Seq. No.      298134
Seq. ID      LIB3150-092-P1-N1-B4
Method       BLASTX
NCBI GI      g461498
BLAST score   227
E value      8.0e-19
```


Match length	92
% identity	58
NCBI Description	ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2) (ALAAT-2) >gi_320619_pir_S28429 alanine transaminase (EC 2.6.1.2) - proso millet >gi_296204_emb_CAA49199_ (X69421) alanine aminotransferase [Panicum miliaceum]
Seq. No.	298135
Seq. ID	LIB3150-092-P1-N1-C3
Method	BLASTX
NCBI GI	g627584
BLAST score	168
E value	6.0e-12
Match length	114
% identity	34
NCBI Description	protein p84 - human >gi_550058 (L36529) protein p84 [Homo sapiens]
Seq. No.	298136
Seq. ID	LIB3150-092-P1-N1-D8
Method	BLASTX
NCBI GI	g1174867
BLAST score	151
E value	1.0e-11
Match length	71
% identity	58
NCBI Description	UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX UBIQUINONE-BINDING PROTEIN QP-C (UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.2 KD PROTEIN) >gi_633687_emb_CAA55862_ (X79275) ubiquinol--cytochrome c reductase [Solanum tuberosum] >gi_1094912_prf_2107179A cytochrome c oxidase:SUBUNIT=8.2kD [Solanum tuberosum]
Seq. No.	298137
Seq. ID	LIB3150-092-P2-K1-A4
Method	BLASTN
NCBI GI	g168492
BLAST score	35
E value	3.0e-10
Match length	39
% identity	97
NCBI Description	Corn histone H3 (H3C3) gene, complete cds
Seq. No.	298138
Seq. ID	LIB3150-092-P2-K1-D12
Method	BLASTN
NCBI GI	g1321660
BLAST score	47
E value	2.0e-17
Match length	71
% identity	92
NCBI Description	Rice mRNA for ascorbate peroxidase, complete cds
Seq. No.	298139
Seq. ID	LIB3150-092-P2-K1-E1
Method	BLASTN

[illegible]

Seq. No.	298167
Seq. ID	LIB3150-095-P1-N1-E1
Method	BLASTN
NCBI GI	g1037129
BLAST score	296
E value	1.0e-166
Match length	400
% identity	94
NCBI Description	(gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize, Tuxpeno CMS 450, mRNA Partial, 1889 nt]

Seq. No. 298168
 Seq. ID LIB3150-095-P1-N1-E12
 Method BLASTX
 NCBI GI g419803
 BLAST score 249
 E value 1.0e-21
 Match length 69
 % identity 68
 NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]

Seq. No. 298169
 Seq. ID LIB3150-095-P2-K1-A7
 Method BLASTN
 NCBI GI g1154858
 BLAST score 45
 E value 2.0e-16
 Match length 57
 % identity 95
 NCBI Description H.vulgare mRNA for L24 ribosomal protein

Seq. No. 298170
 Seq. ID LIB3150-095-P2-K1-H12
 Method BLASTN
 NCBI GI g2341060
 BLAST score 270
 E value 1.0e-150
 Match length 314
 % identity 96
 NCBI Description Zea mays translational initiation factor eIF-4A (tif-4A3) mRNA, complete cds

Seq. No. 298171
 Seq. ID LIB3150-096-P1-N1-D10
 Method BLASTX
 NCBI GI g99771
 BLAST score 335
 E value 2.0e-31
 Match length 109
 % identity 66
 NCBI Description ubiquitin 81-aa extension protein 1 - Arabidopsis thaliana >gi_166934 (J05539) ubiquitin extension protein (UBQ5) [Arabidopsis thaliana]

Seq. No. 298172
 Seq. ID LIB3150-096-P1-N1-D2
 Method BLASTX
 NCBI GI g22168
 BLAST score 231
 E value 9.0e-20
 Match length 62
 % identity 76
 NCBI Description (X15712) adenine nucleotide translocator [Zea mays]

Seq. No. 298173
 Seq. ID LIB3150-096-P1-N1-D3
 Method BLASTX


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Seq. No.      298194
Seq. ID      LIB3150-100-P1-N1-H3
Method       BLASTN
NCBI GI      g1037129
BLAST score   284
E value      1.0e-159
Match length  358
% identity    95
NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
Tuxpeno CMS 450, mRNA Partial, 1889 nt]
```

```
Seq. No.      298195
Seq. ID      LIB3150-100-P1-N1-H5
Method       BLASTX
NCBI GI      g1168609
BLAST score   188
E value      2.0e-14
Match length  71
% identity    51
NCBI Description AUXIN-RESISTANCE PROTEIN AXR1 >gi_479664_pir_S35071
               auxin-resistance protein AXR1 - Arabidopsis thaliana
               >gi_304104 (L13922) ubiquitin-activating enzyme E1
               [Arabidopsis thaliana] >gi_2388579 (AC000098) Match to
               Arabidopsis AXR1 (gb ATHAXR1122). [Arabidopsis thaliana]
               >gi_448755_prf_1917337A ubiquitin-activating enzyme E1
               [Arabidopsis thaliana]
```

Seq. No.	298196
Seq. ID	LIB3150-100-P2-K1-C5
Method	BLASTX
NCBI GI	g445612
BLAST score	149
E value	2.0e-09
Match length	39
% identity	77
NCBI Description	ribosomal protein S19 [Solanum tuberosum]

```
Seq. No.      298197
Seq. ID      LIB3150-100-P2-K1-D1
Method       BLASTX
NCBI GI      g1351270
BLAST score   238
E value      5.0e-20
Match length  53
% identity    89
NCBI Description  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
                >gi_478410_pir_JQ2255 triose-phosphate isomerase (EC
                5.3.1.1) - rice >gi_169821 (M87064) triosephosphate
                isomerase [Oryza sativa]
```

```
Seq. No.      298198
Seq. ID      LIB3150-100-P2-K1-D8
Method       BLASTN
NCBI GI      g22469
BLAST score   61
E-value      9.0e-26
Match length  207
```



```
% identity      81
NCBI Description Maize mRNA for cytoplasmic ribosomal protein S11
```

```
Seq. No.          298199
Seq. ID           LIB3150-100-P2-K1-E6
Method            BLASTX
NCBI GI           g3372518
BLAST score       635
E value           1.0e-66
Match length      123
% identity        97
NCBI Description   (AF050631) invertase [Zea mays]
```

```
Seq. No.          298200
Seq. ID           LIB3150-101-P1-N1-C3
Method            BLASTX
NCBI GI           g1711036
BLAST score       322
E value           5.0e-30
Match length      98
% identity        66
NCBI Description   (U78952) hydroxyproline rich glycoprotein PsHRGP1 [Pisum
                  sativum]
```

Seq. No.	298201
Seq. ID	LIB3150-101-P1-N1-F11
Method	BLASTX
NCBI GI	g1184774
BLAST score	401
E value	3.0e-39
Match length	91
% identity	85
NCBI Description	(U45856) cytosolic glyceraldehyde-3-phosphate dehydrogenase GAPC3 [Zea mays]

Seq. No.	298202
Seq. ID	LIB3150-102-P2-K1-E7
Method	BLASTN
NCBI GI	g2340107
BLAST score	95
E value	4.0e-46
Match length	186
% identity	89
NCBI Description	Zea mays starch branching enzyme IIa (Sbe2a) mRNA, partial cds

```
Seq. No.      298203
Seq. ID       LIB3150-103-P2-K1-A11
Method        BLASTX
NCBI GI       g136063
BLAST score    157
E value       2.0e-10
Match length   35
% identity     91
NCBI Description  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
                >gi_68426_pir_ISZMT triose-phosphate isomerase (EC
                5.3.1.1) - maize >gi_168647 (L00371) triosephosphate
```


BLAST score	220
E value	1.0e-120
Match length	267
% identity	96
NCBI Description	Z.mays (cv DH5xDH7) hsp70-5 mRNA for heat shock protein

```
Seq. No.      298230
Seq. ID      LIB3150-107-P2-K1-B10
Method       BLASTX
NCBI GI      g2492519
BLAST score   161
E value      6.0e-11
Match length  43
% identity    77
NCBI Description  26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT
7) >gi_1395191_dbj_BAA13021_ (D86121) 26S proteasome ATPase
subunit [Spinacia oleracea]
```

Seq. No.	298231
Seq. ID	LIB3150-107-P2-K1-B5
Method	BLASTN
NCBI GI	g498772
BLAST score	143
E value	1.0e-74
Match length	252
% identity	89
NCBI Description	Z.mays (cv DH5xDH7) hsp70-4 mRNA for heat shock protein

Seq. No.	298232
Seq. ID	LIB3150-107-P2-K1-F12
Method	BLASTN
NCBI GI	g2341060
BLAST score	181
E value	3.0e-97
Match length	285
% identity	91
NCBI Description	Zea mays translational initiation factor eIF-4A (tif-4A3) mRNA, complete cds

Seq. No.	298233
Seq. ID	LIB3150-107-P2-K1-H2
Method	BLASTN
NCBI GI	g22324
BLAST score	172
E value	6.0e-92
Match length	212
% identity	95
NCBI Description	Z.mays mRNA for H2B histone (clone cH2B221)

Seq. No.	298234
Seq. ID	LIB3150-108-P1-N1-A11
Method	BLASTX
NCBI GI	g1658313
BLAST score	148
E value	2.0e-09
Match length	102
% identity	39

NCBI Description (Y08987) osr40g2 [Oryza sativa]

```
Seq. No.      298235
Seq. ID      LIB3150-108-P1-N1-C4
Method       BLASTX
NCBI GI      g419803
BLAST score   347
E value      1.0e-32
Match length  122
% identity    60
NCBI Description  zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]
```

```
Seq. No.      298236
Seq. ID      LIB3150-108-P1-N1-C5
Method       BLASTX
NCBI GI      g168664
BLAST score   317
E value      2.0e-29
Match length  65
% identity    88
NCBI Description (M13507) zein protein precursor [Zea mays]
```

```
Seq. No.          298237
Seq. ID           LIB3150-108-P1-N1-E2
Method            BLASTX
NCBI GI           g3335372
BLAST score       172
E value           3.0e-12
Match length      122
% identity        38
NCBI Description   (AC003028) putative SRG1 protein [Arabidopsis thaliana]
```

```
Seq. No.          298238
Seq. ID           LIB3150-108-P1-N1-E5
Method            BLASTX
NCBI GI           g1658313
BLAST score       321
E value           8.0e-30
Match length      91
% identity        34
NCBI Description   (Y08987) osr40g2 [Oryza sativa]
```

```
Seq. No.      298239
Seq. ID      LIB3150-108-P1-N1-G2
Method       BLASTX
NCBI GI      g3746936
BLAST score   175
E value      3.0e-13
Match length  69
% identity    54
NCBI Description (AF091808) actin 1 [Anemia phyllitidis]
```

```
Seq. No.      298240
Seq. ID      LIB3150-108-P1-N1-H7
Method       BLASTX
NCBI GI      q2282584
```


[illegible]

Seq. No.	298247
Seq. ID	LIB3150-109-P2-K1-B5
Method	BLASTX
NCBI GI	g4309698
BLAST score	307
E value	4.0e-28
Match length	130
% identity	56
NCBI Description	(AC006266) putative glucosyltransferase [Arabidopsis thaliana]

Seq. No.	298249
Seq. ID	LIB3150-109-P2-K1-E6
Method	BLASTN
NCBI GI	g168505
BLAST score	41
E value	5.0e-14
Match length	45
% identity	98
NCBI Description	Zea mays histone H3 gene, complete cds

41877


```

Method          BLASTX
NCBI GI         g121472
BLAST score     257
E value         3.0e-22
Match length    110
% identity      45
NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
                  (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                  >gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) -
                  maize >gi_22289_emb_CAA26149_(X02230) glutelin-2 precursor
                  [Zea mays] >gi_22517_emb_CAA37594_(X53514) zein Zc2 [Zea
                  mays] >gi_168485_(M16066) glutelin-2 [Zea mays]

```

Seq. No.	298307
Seq. ID	LIB3151-002-P1-K1-D1
Method	BLASTN
NCBI GI	g168679
BLAST score	40
E value	4.0e-13
Match length	56
% identity	93
NCBI Description	Maize 19 kDa zein mRNA, clone cZ19C2, complete cds. >gi 270687 qb I03334 Sequence 9 from Patent US

```
Seq. No.          298308
Seq. ID           LIB3151-002-P1-K1-E2
Method            BLASTX
NCBI GI           g2832246
BLAST score       367
E value           4.0e-35
Match length      124
% identity        66
NCBI Description   (AF031569) 22-kDa alpha zein 8 [Zea mays]
```

```
Seq. No.      298309
Seq. ID      LIB3151-002-P1-K1-E3
Method       BLASTX
NCBI GI      g121472
BLAST score   184
E value      1.0e-13
Match length  80
% identity    49
NCBI Description  GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
                (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                >gi_72326_pir_ZM19 glutelin 2 precursor (clone pME119) -
                maize >gi_22289_emb_CAA26149_ (X02230) glutelin-2 precursor
                [Zea mays] >gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea
                mays] >gi_168485_ (M16066) glutelin-2 [Zea mays]
```

```
Seq. No.          298310
Seq. ID           LIB3151-002-P1-K1-E5
Method            BLASTX
NCBI GI           g16073
BLAST score       369
E value           2.0e-35
Match length      109
% identity        70
```



```
% identity      55
NCBI Description HMG1/2-LIKE PROTEIN >gi_541981_pir__S39556 HMG protein -
                  fava bean
```

```
Seq. No.      298332
Seq. ID      LIB3151-003-Q1-K1-E6
Method       BLASTX
NCBI GI      g141605
BLAST score   364
E value      6.0e-35
Match length  93
% identity    83
NCBI Description  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
                >gi_72312_pir_ZIZM92 19K zein precursor (clone cz19C2) -
                maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]
```

```
Seq. No.      298333
Seq. ID       LIB3151-003-Q1-K1-F12
Method        BLASTX
NCBI GI       g4586031
BLAST score    280
E value        6.0e-25
Match length   64
% identity     83
NCBI Description (AC007109) unknown protein [Arabidopsis thaliana]
```

Seq. No.	298334
Seq. ID	LIB3151-003-Q1-K1-F5
Method	BLASTN
NCBI GI	g168484
BLAST score	285
E value	1.0e-159
Match length	373
% identity	95
NCBI Description	Maize endosperm glutelin-2 gene, complete cds

Seq. No.	298335
Seq. ID	LIB3151-003-Q1-K1-G4
Method	BLASTN
NCBI GI	g22326
BLAST score	35
E value	3.0e-10
Match length	82
% identity	87
NCBI Description	Z.mays gene for Hageman factor inhibitor

```
Seq. No.          298336
Seq. ID           LIB3151-003-Q1-K1-G7
Method            BLASTX
NCBI GI           g168699
BLAST score       169
E value           3.0e-12
Match length      82
% identity        51
NCBI Description   (M60836) zein [Zea mays]
```

Seq. No. 298337

Seq. ID	LIB3151-003-Q1-K1-G9
Method	BLASTX
NCBI GI	g3757519
BLAST score	383
E value	6.0e-37
Match length	143
% identity	53
NCBI Description	(AC005167) hypothetical protein [Arabidopsis thaliana]

```
Seq. No.      298338
Seq. ID      LIB3151-003-Q1-K1-H11
Method       BLASTX
NCBI GI      g3292831
BLAST score   348
E value      4.0e-33
Match length  104
% identity    62
NCBI Description (AL031018) putative serine/threonine kinase [Arabidopsis
thaliana]
```

```
Seq. No.          298339
Seq. ID           LIB3151-003-Q1-K1-H5
Method            BLASTN
NCBI GI           g22528
BLAST score       125
E value           6.0e-64
Match length      347
% identity        85
NCBI Description   Zea mays mRNA encoding a zein (clone A20)
```

```
Seq. No.          298340
Seq. ID           LIB3151-004-Q1-K1-A11
Method            BLASTN
NCBI GI           g4140643
BLAST score       46
E value           8.0e-17
Match length      57
% identity        95
NCBI Description   Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
                  complete sequence
```

```
Seq. No.      298341
Seq. ID      LIB3151-004-Q1-K1-A5
Method       BLASTX
NCBI GI      g100925
BLAST score   178
E value      4.0e-13
Match length  54
% identity    61
NCBI Description zein, 27K - maize (fragment) >gi_22550_emb_CAA41175_
                (X58197) 27kDa storage protein, zein [Zea mays]
```

```
Seq. No.      298342
Seq. ID      LIB3151-004-Q1-K1-B12
Method       BLASTX
NCBI GI      g121472
BLAST score   222
```



```
E value          4.0e-18
Match length     97
% identity       47
NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
                  (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
>gi_72326_pir_ZM2M19 glutelin 2 precursor (clone pME119) -
maize >gi_22289_emb_CAA26149 (X02230) glutelin-2 precursor
[Zea mays] >gi_22517_emb_CAA37594 (X53514) zein Zc2 [Zea
mays] >gi_168485 (M16066) glutelin-2 [Zea mays]
```

```
Seq. No.      298343
Seq. ID      LIB3151-004-Q1-K1-C11
Method       BLASTX
NCBI GI      g141605
BLAST score   445
E value      2.0e-44
Match length  100
% identity    92
NCBI Description  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
                >gi_72312_pir_ZIZM92 19K zein precursor (clone cZ19C2) -
                maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]
```

Seq. No.	298344
Seq. ID	LIB3151-004-Q1-K1-C5
Method	BLASTX
NCBI GI	g2340108
BLAST score	327
E value	2.0e-30
Match length	109
% identity	60
NCBI Description	(U65948) starch branching enzyme IIa [Zea mays]

Seq. No.	298345
Seq. ID	LIB3151-004-Q1-K1-C8
Method	BLASTX
NCBI GI	g3157932
BLAST score	161
E value	2.0e-11
Match length	78
% identity	45
NCBI Description	(AC002131) Similar to hypothetical protein HYP1 gb_Z97338 from <i>A. thaliana</i> . [<i>Arabidopsis thaliana</i>]

```
Seq. No.      298346
Seq. ID      LIB3151-004-Q1-K1-D9
Method       BLASTX
NCBI GI      g141617
BLAST score   259
E value      2.0e-22
Match length  64
% identity    77
NCBI Description  ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN Zc1)
>gi_100941_pir_S12140 zein Zc1 - maize
>gi_100945_pir_B29017 zein 2 - maize
>gi_22515_emb_CAA37595_(X53515) zein Zc1 [Zea mays]
>gi_168666_(M16460) 16-kDa zein protein [Zea mays]
```


Match length 99
 % identity 61
 NCBI Description (M29628) zein [Zea mays]

Seq. No. 298353
 Seq. ID LIB3151-004-Q1-K1-F11
 Method BLASTX
 NCBI GI g141598
 BLAST score 170
 E value 4.0e-12
 Match length 44
 % identity 75
 NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE ZG99)
 >gi_72313_pir_ZIZM99 19K zein precursor (clone ZG99) -
 maize >gi_22519_emb_CAA24717_ (V01470) zein [Zea mays]
 >gi_22534_emb_CAA24726_ (V01479) zein [Zea mays]

Seq. No. 298354
 Seq. ID LIB3151-004-Q1-K1-F3
 Method BLASTN
 NCBI GI g168484
 BLAST score 161
 E value 2.0e-85
 Match length 348
 % identity 87
 NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 298355
 Seq. ID LIB3151-004-Q1-K1-F9
 Method BLASTX
 NCBI GI g141603
 BLAST score 550
 E value 1.0e-56
 Match length 135
 % identity 87
 NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
 >gi_72311_pir_ZIZM2 19K zein precursor (clone A20) - maize
 >gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]

Seq. No. 298356
 Seq. ID LIB3151-004-Q1-K1-G6
 Method BLASTN
 NCBI GI g4336204
 BLAST score 38
 E value 5.0e-12
 Match length 46
 % identity 96
 NCBI Description Zea mays cytochrome b5 reductase (NFR) mRNA, complete cds

Seq. No. 298357
 Seq. ID LIB3151-004-Q1-K1-H2
 Method BLASTX
 NCBI GI g1345838
 BLAST score 236
 E value 7.0e-20
 Match length 58
 % identity 76


```

Match length      125
% identity        51
NCBI Description  zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)
                  zein Zd1 (19 kDa zein) [Zea mays]

```

```
Seq. No.      298363
Seq. ID      LIB3151-005-Q1-K1-E12
Method       BLASTX
NCBI GI      g266398
BLAST score   349
E value      4.0e-33
Match length  96
% identity    68
NCBI Description TRYPsin/FACTOR XIIIA INHIBITOR PRECURSOR (HAGEMAN FACTOR
INHIBITOR) (CHFI) >gi_68849_pir_TIZM1 trypsin/factor XIIa
inhibitor precursor - maize >gi_22327_emb_CAA37998_
(X54064) corn Hageman factor inhibitor [Zea mays]
```

```
Seq. No.      298364
Seq. ID      LIB3151-005-Q1-K1-E5
Method       BLASTX
NCBI GI      g141608
BLAST score   316
E value      3.0e-29
Match length  118
% identity    60
NCBI Description  ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_S15655
zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa
zein [Zea mays]
```

```
Seq. No.          298365
Seq. ID           LIB3151-005-Q1-K1-E8
Method            BLASTX
NCBI GI           g168701
BLAST score       169
E value           5.0e-12
Match length      53
% identity        58
NCBI Description   (M60837) zein [Zea mays]
```

```
Seq. No.      298366
Seq. ID       LIB3151-005-Q1-K1-E9
Method        BLASTX
NCBI GI       g719291
BLAST score    197
E value        2.0e-15
Match length   83
% identity     46
NCBI Description (U19134) unknown [Arabidopsis thaliana]
               >qi_1095007_prf_2107236A_SABRE_gene [Arabidopsis thaliana]
```

```
Seq. No.      298367
Seq. ID      LIB3151-005-Q1-K1-F1
Method       BLASTN
NCBI GI      g1037129
BLAST score   349
E value      0.0e+00
```



```
BLAST score      351
E value         2.0e-33
Match length    112
% identity      67
NCBI Description 22K zein precursor (clone pZ22.3) - maize >gi_168686
                  (J01246) 26.99 kd zein protein [Zea mays]
```

```
Seq. No.          298373
Seq. ID           LIB3151-005-Q1-K1-H11
Method            BLASTX
NCBI GI           g141597
BLAST score       221
E value           1.0e-32
Match length      130
% identity        62
NCBI Description   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
                  >gi_72314_pir_ZIZM3 19K zein precursor (clone A30) - maize
                  >gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
                  [Zea mays]
```

Seq. No.	298374
Seq. ID	LIB3151-006-Q1-K1-B2
Method	BLASTX
NCBI GI	g141610
BLAST score	184
E value	1.0e-13
Match length	51
% identity	75
NCBI Description	ZEIN-ALPHA PRECURSOR (CLONE Z4)

Seq. No.	298375
Seq. ID	LIB3151-006-Q1-K1-C3
Method	BLASTX
NCBI GI	g168664
BLAST score	282
E value	2.0e-25
Match length	94
% identity	60
NCBI Description	(M13507) zein protein precursor [Zea mays]

```
Seq. No.      298376
Seq. ID      LIB3151-006-Q1-K1-C6
Method       BLASTX
NCBI GI      g141617
BLAST score   271
E value      8.0e-24
Match length  66
% identity    77
NCBI Description  ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
>gi_100941_pir_S12140 zein Zc1 - maize
>gi_100945_pir_B29017 zein 2 - maize
>gi_22515_emb_CAA37595_(X53515) zein Zc1 [Zea mays]
>gi_168666_(M16460) 16-kDa zein protein [Zea mays]
```

Seq. No.	298377
Seq. ID	LIB3151-006-Q1-K1-C9
Method	BLASTX

Seq. No.	298393
Seq. ID	LIB3151-007-Q1-K1-C11
Method	BLASTX
NCBI GI	g141605
BLAST score	177
E value	4.0e-13
Match length	71
% identity	54
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2) >gi_72312_pir_ZIZM92 19K zein precursor (clone cZ19C2) - maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]
Seq. No.	298394
Seq. ID	LIB3151-007-Q1-K1-C12
Method	BLASTN
NCBI GI	g22516
BLAST score	160
E value	8.0e-85
Match length	312
% identity	88
NCBI Description	Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
Seq. No.	298395
Seq. ID	LIB3151-007-Q1-K1-C2
Method	BLASTX
NCBI GI	g141597
BLAST score	230
E value	2.0e-27
Match length	119
% identity	60
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30) >gi_72314_pir_ZIZM3 19K zein precursor (clone A30) - maize >gi_22545_emb_CAA24728_ (V01481) reading frame zein [2] [Zea mays]
Seq. No.	298396
Seq. ID	LIB3151-007-Q1-K1-C5
Method	BLASTX
NCBI GI	g419803
BLAST score	162
E value	6.0e-16
Match length	109
% identity	46
NCBI Description	zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]
Seq. No.	298397
Seq. ID	LIB3151-007-Q1-K1-D11
Method	BLASTN
NCBI GI	g22514
BLAST score	69
E value	6.0e-31
Match length	125
% identity	89
NCBI Description	Maize Zc1 gene for Zein Zc1 (14 kD zein-2)

NCBI GI g168665
 BLAST score 163
 E value 1.0e-86
 Match length 230
 % identity 94
 NCBI Description Maize 16-kDa zein-2 mRNA, complete cds

Seq. No. 298441
 Seq. ID LIB3151-011-Q1-K1-B12
 Method BLASTX
 NCBI GI g121472
 BLAST score 158
 E value 3.0e-11
 Match length 41
 % identity 73
 NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
 (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
 >gi_72326_pir_ZM19 glutelin 2 precursor (clone pME119) -
 maize >gi_22289_emb_CAA26149_(X02230) glutelin-2 precursor
 [Zea mays] >gi_22517_emb_CAA37594_(X53514) zein Zc2 [Zea
 mays] >gi_168485 (M16066) glutelin-2 [Zea mays]

Seq. No. 298442
 Seq. ID LIB3151-011-Q1-K1-B4
 Method BLASTX
 NCBI GI g224508
 BLAST score 270
 E value 6.0e-24
 Match length 79
 % identity 78
 NCBI Description zein A20 [Zea mays]

Seq. No. 298443
 Seq. ID LIB3151-011-Q1-K1-C1
 Method BLASTX
 NCBI GI g168691
 BLAST score 189
 E value 1.0e-14
 Match length 73
 % identity 55
 NCBI Description (M29628) zein [Zea mays]

Seq. No. 298444
 Seq. ID LIB3151-011-Q1-K1-C7
 Method BLASTX
 NCBI GI g419803
 BLAST score 264
 E value 3.0e-23
 Match length 92
 % identity 59
 NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea
 mays]

Seq. No. 298445
 Seq. ID LIB3151-011-Q1-K1-C8
 Method BLASTN
 NCBI GI g1037129

BLAST score 68
E value 3.0e-30
Match length 87
% identity 94
NCBI Description Zea mays zein protein gene, complete cds

Seq. No. 298457
Seq. ID LIB3151-012-Q1-K1-C12
Method BLASTX
NCBI GI g141604
BLAST score 415
E value 1.0e-40
Match length 132
% identity 71
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C1)
>gi_72310_pir_ZIZM91 19K zein precursor (clone cZ19C1) -
maize >gi_168678 (M12146) 19 kDa zein protein [Zea mays]

Seq. No. 298458
Seq. ID LIB3151-012-Q1-K1-C6
Method BLASTX
NCBI GI g224507
BLAST score 173
E value 1.0e-19
Match length 93
% identity 61
NCBI Description zein A1 [Zea mays]

Seq. No. 298459
Seq. ID LIB3151-012-Q1-K1-D12
Method BLASTN
NCBI GI g168677
BLAST score 34
E value 6.0e-10
Match length 50
% identity 94
NCBI Description Maize 19 kDa zein mRNA, clone cZ19C1, complete cds

Seq. No. 298460
Seq. ID LIB3151-012-Q1-K1-D3
Method BLASTX
NCBI GI g141617
BLAST score 229
E value 5.0e-19
Match length 100
% identity 51
NCBI Description ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
>gi_100941_pir_S12140 zein Zc1 - maize
>gi_100945_pir_B29017 zein 2 - maize
>gi_22515_emb_CAA37595 (X53515) zein Zc1 [Zea mays]
>gi_168666 (M16460) 16-kDa zein protein [Zea mays]

Seq. No. 298461
Seq. ID LIB3151-012-Q1-K1-D6
Method BLASTN
NCBI GI g168484
BLAST score 192

